

BLAST2 Search Results

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Retrieval	BLAST2	FASTA	ClustalW	GCG Assembly	Phrap	Translation	BLAST2 Manual
Confidential	- Property of I	ncyte Genomics	, Inc. Life	eSệq Gold 5.1 Ma	y2002		
Program: blastn						RECENT.	

Program: blastn Sequence ID(s):

768320CB1 (LGcompseqsJAN2002) vs. gb129mam

RECEIVED

OCT 15 2002

NCBI-BLASTN 2.0.10 [Aug-26-1999]

TECH CENTER 1600/25

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 768320CB1

(1275 letters)

Database: gb129mam

38,579 sequences; 40,433,150 total letters

Searching........done

Score E Sequences producing significant alignments: (bits) Value **☑** g163228 Bovine inorganic pyrophosphatase mRNA sequence. 1227 0.0 g9957596 Sus scrofa RNA helicase (RHIV-1) mRNA, complete cds. 0.16 g6651078 Ovis aries proviral endogenous Jaagsiekte sheep retr 0.16 ☑ g6851175 Ovis aries Jaagsiekte sheep retrovirus-like element, 0.64 g6651074 Ovis aries proviral endogenous Jaagsiekte sheep retr 0.64

>g163228 Bovine inorganic pyrophosphatase mRNA sequence. Length = 1266

Score = 1227 bits (619), Expect = 0.0
Identities = 847/923 (91%)
Strand = Plus / Plus

Query: 244 ctggtctaatgcaaaaatggagattgctacaaaggaccctttaaaccctattaaacaaga 303

```
Sbjct: 224 ctggtcgaatgcaaaaatggagattgctacaaaggaccctttaaacccaattaaacaaga 283
Query: 304 tgtgaaaaaaggaaaacttcgctatgttgcgaatttgttcccgtataaaggatatatctg 363
        Sbjct: 284 tgtgaagaaaggaaaactccgttatgttgcaaatctgttcccgtataaaggatacatctg 343
Query: 364 gaactatggtgccatccctcagacttgggaagacccagggcacaatgataaacatactgg 423
        Sbjct: 344 gaactacggtgccatccctcagacttgggaagacccaggacacaatgacaaacacactgg 403
Query: 424 ctgttgtggtgacaatgacccaattgatgtgtgtgaaattggaagcaaggtatgtgcaag 483
        Sbjct: 404 ctgttgtggtgacaatgacccaattgatgtgtgtgaaattggaagcaaggtgtgtgcacg 463
Query: 484 aggtgaaataattggcgtgaaagttctaggcatattggctatgattgacgaaggggaaac 543
        Query: 544 cgactggaaagtcattgccattaatgtggatgatcctgatgcagccaattataatgatat 603
        Sbjct: 524 cgactggaaagtcattgccattaatgtggaagatcctgatgcagccaattacaatgatat 583
Query: 604 caatgatgtcaaacggctgaaacctggctacttagaagctactgtggactggtttagaag 663
        Sbjct: 584 taatgatgtcaagcggctgaaacctggctacctggaagctactgtggattggtttaggag 643
Query: 664 gtataaggttcctgatggaaaaccagaaaatgagtttgcgtttaatgcagaatttaaaga 723
        Sbjct: 644 gtacaaggttccagatggaaaacctgaaaatgagtttgctttcaatgcagaatttaaaga 703
Query: 724 taaggactttgccattgatattattaaaagcactcatgaccattggaaagcattagtgac 783
        Sbjct: 704 taagaactttgcaattgacattattgaaagcactcatgactattggagagcattagtgac 763
Query: 784 taagaaaacgaatggaaaaggaatcagttgcatgaatacaactttgtctgagagcccctt 843
        Sbjct: 764 taagaaaactgatggaaaaggaatcagctgcatgaacactacagtgtctgagagcccctt 823
Query: 844 caagtgtgatcctgatgctgccagagccattgtggatgctttaccaccaccctgtgaatc 903
        Sbjct: 824 ccagtgtgatcctgatgctgccaaagccattgtggatgctttaccgccaccatgtgaatc 883
Query: 904 tgcctgcacagtaccaacagacgtggataagtggttccatcaccagaaaaactaatgaga 963
       Sbjct: 884 tgcctgcacaataccaacagatgtggataagtggttccatcaccagaaaaactaaggaaa 943
Query: 964 tttctctggaatacaagctgata 986
       Sbjct: 944 tttctctggaatacaagctgata 966
Score = 52.0 bits (26), Expect = 1e-05
Identities = 32/34 (94%)
Strand = Plus / Plus
Query: 1027 tagtagcttttcaaagctttaaatttgtagaact 1060
        Sbjct: 1005 tagtagcttttccaagctttaaatttatagaact 1038
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```
Score = 48.1 bits (24), Expect = 2e-04
 Identities = 51/60 (85%)
 Strand = Plus / Plus
Query: 1138 tcaactaagataacttttagcacatgcttaaatatcaaagcagttgtcatttggaagtca 1197
           Sbjct: 1108 tcaactaaggtaacatttagttcctgcttaaatatcaaggcggttgtagtttggaagtca 1167
>g9957596 Sus scrofa RNA helicase (RHIV-1) mRNA, complete cds.
           Length = 4024
 Score = 38.2 \text{ bits (19)}, Expect = 0.16
 Identities = 22/23 (95%)
 Strand = Plus / Plus
Query: 864 ccagagccattgtggatgcttta 886
           Sbjct: 1961 ccagagcccttgtggatgcttta 1983
>g6651078 Ovis aries proviral endogenous Jaagsiekte sheep
           retrovirus-like clone enJSRV 5.9A1 protease (pro) gene,
           complete cds; and unknown gene.
           Length = 6696
 Score = 38.2 bits (19), Expect = 0.16
 Identities = 19/19 (100%)
 Strand = Plus / Plus
Query: 257 aaaatggagattgctacaa 275
           Sbjct: 3378 aaaatggagattgctacaa 3396
>g6851175 Ovis aries Jaagsiekte sheep retrovirus-like element,
           complete sequence.
           Length = 7940
 Score = 36.2 \text{ bits (18), Expect} = 0.64
 Identities = 18/18 (100%)
 Strand = Plus / Plus
Query: 258 aaatggagattgctacaa 275
           Sbjct: 3398 aaatggagattgctacaa 3415
>g6651074 Ovis aries proviral endogenous Jaagsiekte sheep
           retrovirus-like clone enJSRV 5f16 Gag (gag), protease
           (pro), and envelope protein (env) genes, complete cds.
           Length = 6916
 Score = 36.2 \text{ bits (18)}, Expect = 0.64
 Identities = 18/18 (100%)
Strand = Plus / Plus
Query: 258
           aaatggagattgctacaa 275
           11111111111111111
Sbjct: 3398 aaatggagattgctacaa 3415
 Database: gb129mam
   Posted date: May 6, 2002 5:07 PM
 Number of letters in database: 40,433,150
 Number of sequences in database: 38,579
```